



## SEQUENCE LISTING

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<120> NOVEL NITRILE HYDRATASE

<130> 018765-218

<140> 10/539,560

<141> 2005-06-16

<150> PCT/JP03/016014

<151> 2003-12-15

<150> JP 2003-379280

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<150> JP 2002-368360

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<160> 142

<170> PatentIn Ver. 3.3

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<213> Pseudonocardia thermophila

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Lys	Glu	Leu	Gly	Ile	Gly	Gly	Leu	Gln	Gly	Glu	Asp	Met	Met	Trp	Val
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Glu	Asn	Thr	Asp	Glu	Val	His	His	Val	Val	Val	Cys	Thr	Leu	Cys	Ser
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 Pro Gln Tyr Arg Ser Arg Val Val Arg Glu Pro Arg Gln Leu Leu Lys  
 130 135 140  
 Glu Glu Phe Gly Phe Glu Val Pro Pro Ser Lys Glu Ile Lys Val Trp  
 145 150 155 160  
 Asp Ser Ser Ser Glu Met Arg Phe Val Val Leu Pro Gln Arg Pro Ala  
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 Asp Glu Phe Arg Phe Gly Ile Glu Gln Met Asn Pro Ala Glu Tyr Leu  
 50 55 60  
 Glu Ser Pro Tyr Tyr Trp His Trp Ile Arg Thr Tyr Ile His His Gly  
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 Val Arg Thr Gly Lys Ile Asp Leu Glu Glu Leu Glu Arg Arg Thr Gln  
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 Tyr Tyr Arg Glu Asn Pro Asp Ala Pro Leu Pro Glu His Glu Gln Lys  
 100 105 110  
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 Ala Ser Arg Glu Val Asp Arg Pro Pro Lys Phe Lys Glu Gly Asp Val  
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 Tyr Val Arg Gly Lys Thr Gly Thr Val Val Lys His His Gly Ala Tyr  
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Ile Tyr Pro Asp Thr Ala Gly Asn Gly Leu Gly Glu Cys Pro Glu His  
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Leu Tyr Thr Val Arg Phe Thr Ala Gln Glu Leu Trp Gly Pro Glu Gly  
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<213> *Pseudonocardia thermophila*

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gactccagct	ccgagatgcg	cttcgtcgct	ctcccgacgc	gccccgcggg	caccgacggg	540
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<213> *Pseudonocardia thermophila*

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<213> *Pseudonocardia thermophila*

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 35           40           45

Ala Leu Ala Val Ala Ala Cys Arg Ala Gly Arg Phe Glu Trp Lys Gln
 50           55           60

Leu Gln Gln Ala Leu Ile Ser Ser Ile Gly Glu Trp Glu Arg Thr His
 65           70           75           80

Asp Leu Asp Asp Pro Ser Trp Ser Tyr Tyr Glu His Phe Val Ala Ala
          85           90           95

Leu Glu Ser Val Leu Gly Glu Glu Gly Ile Val Glu Pro Glu Ala Leu
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primer

<400> 78  
gacgagtccc gggttcggc

18

<210> 79  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 79  
tggcacttta tccgcacc

18

<210> 80  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 80  
atcgaggccg tcaaccag

18

<210> 81  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 81  
atcgagctcg tcaaccag

18

<210> 82  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer  
  
<400> 82  
atcgagctcg tcaaccag 18  
  
<210> 83  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
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<223> Description of Artificial Sequence: Synthetic primer  
  
<400> 83  
atcgaggctcg tcaaccag 18  
  
<210> 84  
<211> 18  
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<213> Artificial Sequence  
  
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<223> Description of Artificial Sequence: Synthetic primer  
  
<400> 84  
ggcggggcgc ccgcaagc 18  
  
<210> 85  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
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<223> Description of Artificial Sequence: Synthetic primer  
  
<400> 85  
ggcggggtgc ccgcaagc 18  
  
<210> 86  
<211> 18  
<212> DNA  
<213> Artificial Sequence  
  
<220>  
<223> Description of Artificial Sequence: Synthetic primer  
  
<400> 86  
ggcgggtcgc ccgcaagc 18

<210> 87  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 87  
gtggtggggt tctccacc 18

<210> 88  
<211> 18  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 88  
cgcgcgctgt acgtgcgc 18

<210> 89  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 89  
cgcgcggtgt acgtgcgc 18

<210> 90  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 90  
aacggcgagg gcgagtgc 18

<210> 91  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 91  
aacggcgatg gcgagtgc 18

<210> 92  
<211> 18  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Synthetic primer

<400> 92  
aacggcaagg gcgagtgc 18

<210> 93  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
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<400> 93  
aacggccggg gcgagtgc 18

<210> 94  
<211> 18  
<212> DNA  
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<220>  
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<400> 94  
aacggcaacg gcgagtgc 18

<210> 95  
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<212> DNA  
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<220>  
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<400> 95  
aacggctcgg gcgagtgc

18

<210> 96  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 96  
aacggcgggg gcgagtgc

18

<210> 97  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<400> 97  
tactacggct gctgggag

18

<210> 98  
<211> 205  
<212> PRT  
<213> Pseudonocardia thermophila

<400> 98  
Met Thr Glu Asn Ile Leu Arg Lys Ser Asp Glu Glu Ile Gln Lys Glu  
1 5 10 15  
Ile Thr Ala Arg Val Lys Ala Leu Glu Ser Met Leu Ile Glu Gln Gly  
20 25 30  
Ile Leu Thr Thr Ser Met Ile Asp Arg Met Ala Glu Ile Tyr Glu Asn  
35 40 45  
Glu Val Gly Pro His Leu Gly Ala Lys Val Val Val Lys Ala Trp Thr  
50 55 60  
Asp Pro Glu Phe Lys Lys Arg Leu Leu Ala Asp Gly Thr Glu Ala Cys  
65 70 75 80  
Lys Glu Leu Gly Ile Gly Gly Leu Gln Gly Glu Asp Met Met Trp Val  
85 90 95  
Glu Asn Thr Asp Glu Val His His Val Val Val Cys Thr Leu Cys Ser  
100 105 110

Cys	Tyr	Pro	Trp	Pro	Val	Leu	Gly	Leu	Pro	Pro	Asn	Trp	Phe	Lys	Glu
		115					120					125			
Pro	Gln	Tyr	Arg	Ser	Arg	Val	Val	Arg	Glu	Pro	Arg	Gln	Leu	Leu	Lys
	130					135					140				
Glu	Glu	Phe	Gly	Phe	Glu	Val	Pro	Pro	Ser	Lys	Glu	Ile	Lys	Val	Trp
145					150					155					160
Asp	Ser	Ser	Ser	Glu	Met	Arg	Phe	Val	Val	Leu	Pro	Gln	Arg	Pro	Ala
				165					170					175	
Gly	Thr	Asp	Gly	Trp	Ser	Glu	Glu	Glu	Leu	Ala	Thr	Leu	Val	Thr	Arg
			180					185					190		
Glu	Ser	Met	Ile	Gly	Val	Glu	Pro	Ala	Lys	Ala	Val	Ala			
		195					200					205			

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<210> 99
<211> 233
<212> PRT
<213> Pseudonocardia thermophila
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<400>	99															
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1				5					10					15		
Asn	Arg	Pro	Ala	Asp	Glu	Pro	Val	Phe	Arg	Ala	Glu	Trp	Glu	Lys	Val	
			20					25					30			
Ala	Phe	Ala	Met	Phe	Pro	Ala	Thr	Phe	Arg	Ala	Gly	Phe	Met	Gly	Leu	
		35					40					45				
Asp	Glu	Phe	Arg	Phe	Gly	Ile	Glu	Gln	Met	Asn	Pro	Ala	Glu	Tyr	Leu	
	50					55					60					
Glu	Ser	Pro	Tyr	Tyr	Trp	His	Trp	Ile	Arg	Thr	Tyr	Ile	His	His	Gly	
65					70				75						80	
Val	Arg	Thr	Gly	Lys	Ile	Asp	Leu	Glu	Glu	Leu	Glu	Arg	Arg	Thr	Gln	
				85					90					95		
Tyr	Tyr	Arg	Glu	Asn	Pro	Asp	Ala	Pro	Leu	Pro	Glu	His	Glu	Gln	Lys	
			100					105					110			
Pro	Glu	Leu	Ile	Glu	Phe	Val	Asn	Gln	Ala	Val	Tyr	Gly	Gly	Leu	Pro	
		115					120					125				
Ala	Ser	Arg	Glu	Val	Asp	Arg	Pro	Pro	Lys	Phe	Lys	Glu	Gly	Asp	Val	
	130					135					140					
Val	Arg	Phe	Ser	Thr	Ala	Ser	Pro	Lys	Gly	His	Ala	Arg	Arg	Ala	Arg	
145					150					155					160	
Tyr	Val	Arg	Gly	Lys	Thr	Gly	Thr	Val	Val	Lys	His	His	Gly	Ala	Tyr	
				165					170					175		

Ile Tyr Pro Asp Thr Ala Gly Asn Gly Leu Gly Glu Cys Pro Glu His  
 180 185 190

Leu Tyr Thr Val Arg Phe Thr Ala Gln Glu Leu Trp Gly Pro Glu Gly  
 195 200 205

Asp Pro Asn Ser Ser Val Tyr Tyr Asp Cys Trp Glu Pro Tyr Ile Glu  
 210 215 220

Leu Val Asp Thr Lys Ala Ala Ala  
 225 230

<210> 100

<211> 618

<212> DNA

<213> *Pseudonocardia thermophila*

<400> 100

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atgaccgaga acatcctgcg caagtcggac gaggagatcc agaaggagat caccggcgcg 60
gtcaaggccc tggagtcgat gtcctatcgaa cagggcatcc tcaccacgtc gatgatcgac 120
cggatggccg agatctacga gaacgaggtc ggcccgacac tcggcgcgaa ggtcgtcgtg 180
aaggcctgga ccgacccgga gttcaagaag cgtctgctcg ccgacggcac cgaggcctgc 240
aaggagctcg gcatcggcgg cctgcagggc gaggacatga tgtgggtgga gaacaccgac 300
gaggtccacc acgtcgctcg gtgcacgctc tgctcctgct acccgaggcc ggtgctgggg 360
ctgccgccga actggttcaa ggagccgcag taccgctccc gcgtggtgcg tgagcccccg 420
cagctgctca aggaggagtt cggcttcgag gtcccgccga gcaaggagat caaggtctgg 480
gactccagct ccgagatgcg cttcgtcgct ctcccgagc gccccgcggg caccgacggg 540
tggagcgagg aggagctcgc caccctcgct acccgcgagt cgatgatcgg cgtcgaaccg 600
gcgaaggcgg tcgctgta 618
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<210> 101

<211> 702

<212> DNA

<213> *Pseudonocardia thermophila*

<400> 101

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atgaacggcg tgtacgacgt cggcggcacc gatgggctgg gcccgatcaa ccggcccgcg 60
gacgaaccgg tcttccgcgc cgagtgggag aaggtcgctg tcgcgatgtt cccggcgacg 120
ttccgggccc gcttcatggg cctggacgag ttccgggtcg gcatcgagca gatgaaccgg 180
gccgagtacc tcgagtcgcc gtactactgg cactggatcc gcacctacat ccaccacggc 240
gtccgcaccg gcaagatcga tctcgaggag ctggagcgcc gcacgcagta ctaccgggag 300
aaccgccgacg ccccgctgcc cgagcacgag cagaagccgg agttgatcga gttcgtcaac 360
caggccgtct acggcgggct gcccgcaagc cgggaggtcg accgaccgcc caagttcaag 420
gagggcgacg tgggtgcggt ctccaccgcg agcccgaagg gccacgcccg gcgcgcgcgg 480
tacgtgcgcg gcaagaccgg gacggtggtc aagcaccacg gcgcgtacat ctaccgggac 540
accgccggca acggcctggg cgagtgcgcc gagcacctct acaccgtccg cttcacggcc 600
caggagctgt gggggccgga aggggacccg aactccagcg tctactacga ctgctgggag 660
ccctacatcg agctcgtcga cacgaaggcg gccgcggcat ga 702
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<210> 102

<211> 144

<212> PRT

<213> *Pseudonocardia thermophila*

&lt;400&gt; 102

Met Ser Ala Glu Ala Lys Val Arg Leu Lys His Cys Pro Thr Ala Glu  
 1 5 10 15

Asp Arg Ala Ala Ala Asp Ala Leu Leu Ala Gln Leu Pro Gly Gly Asp  
 20 25 30

Arg Ala Leu Asp Arg Gly Phe Asp Glu Pro Trp Gln Leu Arg Ala Phe  
 35 40 45

Ala Leu Ala Val Ala Ala Cys Arg Ala Gly Arg Phe Glu Trp Lys Gln  
 50 55 60

Leu Gln Gln Ala Leu Ile Ser Ser Ile Gly Glu Trp Glu Arg Thr His  
 65 70 75 80

Asp Leu Asp Asp Pro Ser Trp Ser Tyr Tyr Glu His Phe Val Ala Ala  
 85 90 95

Leu Glu Ser Val Leu Gly Glu Glu Gly Ile Val Glu Pro Glu Ala Leu  
 100 105 110

Asp Glu Arg Thr Ala Glu Val Leu Ala Asn Pro Pro Asn Lys Asp His  
 115 120 125

His Gly Pro His Leu Glu Pro Val Ala Val His Pro Ala Val Arg Ser  
 130 135 140

&lt;210&gt; 103

&lt;211&gt; 435

&lt;212&gt; DNA

<213> *Pseudonocardia thermophila*

&lt;400&gt; 103

rtgagcgccg aggcgaaggt ccgcctgaag cactgccccca cggccgagga ccgggcgggcg 60  
 gccgacgcgc tgctcgcgca gctgcccggc ggcgaccgcg cgctcgaccg cggtctcgac 120  
 gagccgtggc agctgcgggc gttcgcgctg gcggtcgcgg cgtgcagggc gggccgggttc 180  
 gaggggaagc agctgcagca ggcgctgacg tcctcgatcg gggagtggga gcgcaccac 240  
 gatctcgacg atccgagctg gtcctactac gagcacttcg tcgccgcgct ggaatccgtg 300  
 ctcggcgagg aagggatcgt cgagccggag gcgctggacg agcgcaccgc ggaggtcttg 360  
 gcccaaccgc cgaacaagga tcaccatgga ccgcatctgg agcccgtcgc ggtccaccgc 420  
 gccgtgcggt cctga 435

&lt;210&gt; 104

&lt;211&gt; 1315

&lt;212&gt; DNA

<213> *Rhodococcus rhodochrous*

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1) .. (690)

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (704)..(1315)

&lt;400&gt; 104

atg gat ggt atc cac gac aca ggc ggc atg acc gga tac gga ccg gtc	48
Met Asp Gly Ile His Asp Thr Gly Gly Met Thr Gly Tyr Gly Pro Val	
1 5 10 15	
ccc tat cag aag gac gag ccc ttc ttc cac tac gag tgg gag ggt cgg	96
Pro Tyr Gln Lys Asp Glu Pro Phe Phe His Tyr Glu Trp Glu Gly Arg	
20 25 30	
acc ctg tca att ctg act tgg atg cat ctc aag ggc ata tcg tgg tgg	144
Thr Leu Ser Ile Leu Thr Trp Met His Leu Lys Gly Ile Ser Trp Trp	
35 40 45	
gac aag tcg cgg ttc ttc cgg gag tcg atg ggg aac gaa aac tac gtc	192
Asp Lys Ser Arg Phe Phe Arg Glu Ser Met Gly Asn Glu Asn Tyr Val	
50 55 60	
aac gag att cgc aac tcg tac tac acc cac tgg ctg agt gcg gca gaa	240
Asn Glu Ile Arg Asn Ser Tyr Tyr Thr His Trp Leu Ser Ala Ala Glu	
65 70 75 80	
cgt atc ctc gtc gcc gac aag atc atc acc gaa gaa gag cga aag cac	288
Arg Ile Leu Val Ala Asp Lys Ile Ile Thr Glu Glu Glu Arg Lys His	
85 90 95	
cgt gtg caa gag atc ctt gag ggt cgg tac acg gac agg aag ccg tcg	336
Arg Val Gln Glu Ile Leu Glu Gly Arg Tyr Thr Asp Arg Lys Pro Ser	
100 105 110	
cgg aag ttc gat ccg gcc cag atc gag aag gcg atc gaa cgg ctt cac	384
Arg Lys Phe Asp Pro Ala Gln Ile Glu Lys Ala Ile Glu Arg Leu His	
115 120 125	
gag ccc cac tcc cta gcg ctt cca gga gcg gag ccg agt ttc tct ctc	432
Glu Pro His Ser Leu Ala Leu Pro Gly Ala Glu Pro Ser Phe Ser Leu	
130 135 140	
ggt gac aag atc aaa gtg aag agt atg aac ccg ctg gga cac aca cgg	480
Gly Asp Lys Ile Lys Val Lys Ser Met Asn Pro Leu Gly His Thr Arg	
145 150 155 160	
tgc ccg aaa tat gtg cgg aac aag atc ggg gaa atc gtc gcc tac cac	528
Cys Pro Lys Tyr Val Arg Asn Lys Ile Gly Glu Ile Val Ala Tyr His	
165 170 175	
ggc tgc cag atc tat ccc gag agc agc tcc gcc ggc ctc ggc gac gat	576
Gly Cys Gln Ile Tyr Pro Glu Ser Ser Ser Ala Gly Leu Gly Asp Asp	
180 185 190	
cct cgc ccg ctc tac acg gtc gcg ttt tcc gcc cag gaa ctg tgg ggc	624
Pro Arg Pro Leu Tyr Thr Val Ala Phe Ser Ala Gln Glu Leu Trp Gly	
195 200 205	

gac gac gga aac ggg aaa gac gta gtg tgc gtc gat ctc tgg gaa ccg	672
Asp Asp Gly Asn Gly Lys Asp Val Val Cys Val Asp Leu Trp Glu Pro	
210 215 220	
tac ctg atc tct gcg tgaaaggaat acgata gtg agc gag cac gtc aat aag	724
Tyr Leu Ile Ser Ala Met Ser Glu His Val Asn Lys	
225 1 5	
tac acg gag tac gag gca cgt acc aag gcg atc gaa acc ttg ctg tac	772
Tyr Thr Glu Tyr Glu Ala Arg Thr Lys Ala Ile Glu Thr Leu Leu Tyr	
10 15 20	
gag cga ggg ctc atc acg ccc gcc gcg gtc gac cga gtc gtt tcg tac	820
Glu Arg Gly Leu Ile Thr Pro Ala Ala Val Asp Arg Val Val Ser Tyr	
25 30 35	
tac gag aac gag atc ggc ccg atg ggc ggt gcc aag gtc gtg gcc aag	868
Tyr Glu Asn Glu Ile Gly Pro Met Gly Gly Ala Lys Val Val Ala Lys	
40 45 50 55	
tcc tgg gtg gac cct gag tac cgc aag tgg ctc gaa gag gac gcg acg	916
Ser Trp Val Asp Pro Glu Tyr Arg Lys Trp Leu Glu Glu Asp Ala Thr	
60 65 70	
gcc gcg atg gcg tca ttg ggc tat gcc ggt gag cag gca cac caa att	964
Ala Ala Met Ala Ser Leu Gly Tyr Ala Gly Glu Gln Ala His Gln Ile	
75 80 85	
tcg gcg gtc ttc aac gac tcc caa acg cat cac gtg gtg gtg tgc act	1012
Ser Ala Val Phe Asn Asp Ser Gln Thr His His Val Val Val Cys Thr	
90 95 100	
ctg tgt tcg tgc tat ccg tgg ccg gtg ctt ggt ctc ccg ccc gcc tgg	1060
Leu Cys Ser Cys Tyr Pro Trp Pro Val Leu Gly Leu Pro Pro Ala Trp	
105 110 115	
tac aag agc atg gag tac cgg tcc cga gtg gta gcg gac cct cgt gga	1108
Tyr Lys Ser Met Glu Tyr Arg Ser Arg Val Val Ala Asp Pro Arg Gly	
120 125 130 135	
gtg ctc aag cgc gat ttc ggt ttc gac atc ccc gat gag gtg gag gtc	1156
Val Leu Lys Arg Asp Phe Gly Phe Asp Ile Pro Asp Glu Val Glu Val	
140 145 150	
agg gtt tgg gac agc agc tcc gaa atc cgc tac atc gtc atc ccg gaa	1204
Arg Val Trp Asp Ser Ser Ser Glu Ile Arg Tyr Ile Val Ile Pro Glu	
155 160 165	
cgg ccg gcc ggc acc gac ggt tgg tcc gag gag gag ctg acg aag ctg	1252
Arg Pro Ala Gly Thr Asp Gly Trp Ser Glu Glu Glu Leu Thr Lys Leu	
170 175 180	
gtg agc cgg gac tcg atg atc ggt gtc agt aat gcg ctc aca ccg cag	1300
Val Ser Arg Asp Ser Met Ile Gly Val Ser Asn Ala Leu Thr Pro Gln	
185 190 195	

gaa gtg atc gta tga  
 Glu Val Ile Val  
 200

1315

<210> 105  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 primer

<400> 105  
 ccggaattcg aaaggaatga ggaaatgga

29

<210> 106  
 <211> 28  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 primer

<400> 106  
 aaaaagtact catacgatca cttcctgc

28

<210> 107  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 primer

<400> 107  
 gttttcccag tcacgac

17

<210> 108  
 <211> 20  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 primer

<400> 108  
 ggccagtgcc tagcttacat

20

<210> 109  
 <211> 17  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 primer

<400> 109  
 caggaaacag ctatgac

17

<210> 110  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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 primer

<220>  
 <221> modified\_base  
 <222> (14)..(16)  
 <223> a, c, g, t, unknown or other

<400> 110  
 gggcatatcg tggnnngaca agtcgcggt

29

<210> 111  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 primer

<220>  
 <221> modified\_base  
 <222> (7)..(9)  
 <223> a, c, g, t, unknown or other

<400> 111  
 ctcaccnnnt cgatgac

18

<210> 112  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic  
 primer



<220>  
<221> modified\_base  
<222> (7)..(9)  
<223> a, c, g, t, unknown or other

<400> 112  
tacgagnnng aggtcggc

18

<210> 113  
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<212> DNA  
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<220>  
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primer

<220>  
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<222> (7)..(9)  
<223> a, c, g, t, unknown or other

<400> 113  
aagaagnnnc tgctcgcc

18

<210> 114  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<220>  
<221> modified\_base  
<222> (7)..(9)  
<223> a, c, g, t, unknown or other

<400> 114  
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18

<210> 115  
<211> 18  
<212> DNA  
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<220>  
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primer

<220>  
<221> modified\_base  
<222> (7)..(9)  
<223> a, c, g, t, unknown or other

<400> 115  
ctcgccnnnc tcgtcact 18

<210> 116  
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<220>  
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primer

<220>  
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<222> (7)..(9)  
<223> a, c, g, t, unknown or other

<400> 116  
aaggcgnnng cgtgagcg 18

<210> 117  
<211> 18  
<212> DNA  
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<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<220>  
<221> modified\_base  
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<223> a, c, g, t, unknown or other

<400> 117  
ggcggcnnng atgggctg 18

<210> 118  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<220>  
<221> modified\_base  
<222> (7)..(9)  
<223> a, c, g, t, unknown or other

<400> 118  
gagaagnnng cgttcgcg 18

<210> 119  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
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primer

<220>  
<221> modified\_base  
<222> (7)..(9)  
<223> a, c, g, t, unknown or other

<400> 119  
aagtcnnnt tcgcgatg

18

<210> 120  
<211> 18  
<212> DNA  
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<220>  
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primer

<220>  
<221> modified\_base  
<222> (7)..(9)  
<223> a, c, g, t, unknown or other

<400> 120  
gcgatgnnnc cggcgacg

18

<210> 121  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<220>  
<221> modified\_base  
<222> (7)..(9)  
<223> a, c, g, t, unknown or other

<400> 121  
ccggcgnnnt tccgggcc

18

<210> 122  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<220>  
<221> modified\_base  
<222> (7)..(9)  
<223> a, c, g, t, unknown or other

<400> 122  
gcgacgnnnc gggccggc

18

<210> 123  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence: Synthetic  
primer

<220>  
<221> modified\_base  
<222> (7)..(9)  
<223> a, c, g, t, unknown or other

<400> 123  
ggcttcnnng gcctggac

18

<210> 124  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
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primer

<220>  
<221> modified\_base  
<222> (7)..(9)  
<223> a, c, g, t, unknown or other

<400> 124  
atgggcnnng acgagttc

18

<210> 125  
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primer

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 1 5 10 15  
 Pro Tyr Gln Lys Asp Glu Pro Phe Phe His Tyr Glu Trp Glu Gly Arg  
 20 25 30  
 Thr Leu Ser Ile Leu Thr Trp Met His Leu Lys Gly Ile Ser Trp Trp  
 35 40 45  
 Asp Lys Ser Arg Phe Phe Arg Glu Ser Met Gly Asn Glu Asn Tyr Val  
 50 55 60  
 Asn Glu Ile Arg Asn Ser Tyr Tyr Thr His Trp Leu Ser Ala Ala Glu  
 65 70 75 80

Arg Ile Leu Val Ala Asp Lys Ile Ile Thr Glu Glu Glu Arg Lys His  
85 90 95

Arg Val Gln Glu Ile Leu Glu Gly Arg Tyr Thr Asp Arg Lys Pro Ser  
100 105 110

Arg Lys Phe Asp Pro Ala Gln Ile Glu Lys Ala Ile Glu Arg Leu His  
115 120 125

Glu Pro His Ser Leu Ala Leu Pro Gly Ala Glu Pro Ser Phe Ser Leu  
130 135 140

Gly Asp Lys Ile Lys Val Lys Ser Met Asn Pro Leu Gly His Thr Arg  
145 150 155 160

Cys Pro Lys Tyr Val Arg Asn Lys Ile Gly Glu Ile Val Ala Tyr His  
165 170 175

Gly Cys Gln Ile Tyr Pro Glu Ser Ser Ser Ala Gly Leu Gly Asp Asp  
180 185 190

Pro Arg Pro Leu Tyr Thr Val Ala Phe Ser Ala Gln Glu Leu Trp Gly  
195 200 205

Asp Asp Gly Asn Gly Lys Asp Val Val Cys Val Asp Leu Trp Glu Pro  
210 215 220

Tyr Leu Ile Ser Ala  
225

<210> 141

<211> 203

<212> PRT

<213> Rhodococcus rhodochrous

<400> 141

Met Ser Glu His Val Asn Lys Tyr Thr Glu Tyr Glu Ala Arg Thr Lys  
1 5 10 15

Ala Ile Glu Thr Leu Leu Tyr Glu Arg Gly Leu Ile Thr Pro Ala Ala  
20 25 30

Val Asp Arg Val Val Ser Tyr Tyr Glu Asn Glu Ile Gly Pro Met Gly  
35 40 45

Gly Ala Lys Val Val Ala Lys Ser Trp Val Asp Pro Glu Tyr Arg Lys  
50 55 60

Trp Leu Glu Glu Asp Ala Thr Ala Ala Met Ala Ser Leu Gly Tyr Ala  
65 70 75 80

Gly Glu Gln Ala His Gln Ile Ser Ala Val Phe Asn Asp Ser Gln Thr  
85 90 95

His	His	Val	Val	Cys	Thr	Leu	Cys	Ser	Cys	Tyr	Pro	Trp	Pro	Val
		100					105					110		

Leu Gly Leu Pro Pro Ala Trp Tyr Lys Ser Met Glu Tyr Arg Ser Arg  
           115                          120                          125  
 Val Val Ala Asp Pro Arg Gly Val Leu Lys Arg Asp Phe Gly Phe Asp  
       130                          135                          140  
 Ile Pro Asp Glu Val Glu Val Arg Val Trp Asp Ser Ser Ser Glu Ile  
 145                          150                          155                          160  
 Arg Tyr Ile Val Ile Pro Glu Arg Pro Ala Gly Thr Asp Gly Trp Ser  
                           165                          170                          175  
 Glu Glu Glu Leu Thr Lys Leu Val Ser Arg Asp Ser Met Ile Gly Val  
                           180                          185                          190  
 Ser Asn Ala Leu Thr Pro Gln Glu Val Ile Val  
           195                          200

<210> 142

<211> 11

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic peptide

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<221> MOD\_RES

<222> (1)

<223> variable amino acid

<220>

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<222> (3)

<223> Ser or Thr

<220>

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<223> variable amino acid

<220>

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<222> (5)

<223> cysteine sulfinic acid

<220>

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<222> (8)..(11)

<223> variable amino acid

&lt;400&gt; 142

Xaa Cys Xaa Leu Cys Ser Cys Xaa Xaa Xaa Xaa  
1 5 10